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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2003, 07:06:05 ; Search time 28 Seconds  
(without alignments)  
1294.381 Million cell updates/sec

File: US-10-091-628-2  
Perfect score: 1979  
Sequence: 1 MRANCSSSSACFANSEBEL.....PGPMDCRALPFGVGHITSCE 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 73:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	884	44.7	348	2 A49876	Na+-dependent bile
2	860.5	43.5	348	2 I38655	ileal sodium-depen
3	559.5	28.3	362	2 A41601	Na+/taurocholate t
4	553	27.9	349	2 I55601	Na+/taurocholate co
5	333.5	16.9	477	2 S01696	gene p3 protein -
6	325	16.4	321	2 E69902	probable sodium-de
7	301.5	15.2	305	2 D90031	hypothetical prote
8	299.5	15.1	318	2 A32295	sodium/bile acid c
9	299.5	15.1	323	2 B3757	sodium-dependent t
10	284	14.4	338	2 T02645	hypothetical prote
11	269.5	13.6	311	2 F83236	probable transport
12	266.5	13.5	315	2 B81168	transporter NMB070
13	265.5	13.4	315	2 E81937	probable transmem
14	257.5	13.0	297	2 D83438	probable transport
15	250	12.6	297	2 E70482	Na(+)-dependent tr
16	238.5	12.1	292	2 S75443	p3 protein - synec
17	223	11.3	207	2 G98166	probable transport
18	223	11.3	207	2 AH3120	sodium bile acid s
19	222.5	11.2	318	2 G81995	probable transmem
20	219.5	11.1	298	2 AF2462	hypothetical prote
21	180.5	9.1	182	2 I54222	housekeeping prote
22	171	8.6	460	2 T04579	hypothetical prote
23	156	7.9	379	2 T06610	hypothetical prote
24	142	7.2	344	2 T34981	probable integral
25	125	6.3	409	2 I40489	hypothetical prote
26	121.5	6.1	324	2 H72285	conserved hypothet
27	121	6.1	612	2 T40506	major facilitator
28	120	6.1	716	2 AB1070	probable carbon st
29	117	5.9	721	2 S56580	carbon starvation

ALIGNMENTS

RESULT 1

A49876  
Na+-dependent bile acid transporter, ileal - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 30-Jun-1995 #sequence\_revision 30-Jun-1995-#text\_change/ 05-Nov-1999  
C:Accession: A49876

B:Wong, M.H.; Oelkers, P.; Craddock, A.L.; Dawson, P.A.

J. Biol. Chem. 269:1340-1347, 1994

Abstract: Expression cloning and characterization of the hamster ileal sodium-dependent

A:Reference number: A49876; MUID:94117449; PMID:8288599

A:Accession: A49876

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-348 <WON>

A:Cross-references: GB:U02028; NID:G455032; PIDN:AAA18640.1; PID:G455033

C:Keywords: transmembrane protein

Query Match 44.7%; Score 884; DB 2; Length 348;  
Best Local Similarity 46.9%; Pred. No. 2.6e-65;  
Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy	7	SSSACPANSS--EBELPVGLEVHGN--LELVFTVVSTVMMGLMFLSCSVSEIRKLWSHI	62
Db	3	SSSACPANSS--EBELPVGLEVHGN--LELVFTVVSTVMMGLMFLSCSVSEIRKLWSHI	62
Qy	63	RRPWGIAVGLLCQGLMPFTAYLLAISPLKPAQIAVLINGCCPGGTISNIFFWVDG	122
Db	63	RRPWGIAVGLLCQGLMPFTAYLLAISPLKPAQIAVLINGCCPGGTISNIFFWVDG	122
Qy	123	MDLSISMTTCTVAALGMWPLCIYLYTWSLSQQNLITIPYONIGITLVCLTIPVAFGVV	182
Db	123	MDLSISMTTCTVAALGMWPLCIYLYTWSLSQQNLITIPYONIGITLVCLTIPVAFGVV	182
Qy	183	NYRWPKOSKILKIGAVGVGVLVAVAGVVLVAKGSWNSDITLLTISFIPPLIGHVTGF	242
Db	183	NYRWPKOSKILKIGAVGVGVLVAVAGVVLVAKGSWNSDITLLTISFIPPLIGHVTGF	242
Qy	243	LLALFTQSWORCRTISLETQAQNIQMCITMLQSLFTHAHLVQMLSPFLAFLGLFOLDGF	302
Db	243	LLALFTQSWORCRTISLETQAQNIQMCITMLQSLFTHAHLVQMLSPFLAFLGLFOLDGF	302
Qy	303	LIVAAQTYKRLNKGKNGSGTEVCHTRKS--TSSRETNAPLEVNEE	350
Db	303	LIVAAQTYKRLNKGKNGSGTEVCHTRKS--TSSRETNAPLEVNEE	350

RESULT 2

I38655  
ileal sodium-dependent bile acid transporter - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jul-2000  
C:Accession: I38655

R. Wong, M.H.; Oelkers, P.; Dawson, P.A.  
 J. Biol. Chem. 270: 27228-27234, 1995  
 A; Title: Identification of a mutation in the ileal sodium-dependent bile acid transporter  
 A; Reference number: I38655; MUID: 96070831; PMID: 7592981  
 A; Accession: I38655  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-348 <RES>  
 A; Cross-references: EMBL:U10417; NID:g2623285; PIDN:AAC51870.1; PID:g5953399  
 A; Experimental source: Crohn's disease patient (heterozygous)  
 A; Note: the wild type is shown; a form with 290-Ser was deficient in transport activity  
 C; Genetics:  
 A; Gene: SLC15-A2

[illegible]

RESULT 3  
A41601  
Na+/taurocholate transport protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 16-Feb-1997  
C:Accession: A41601  
Gaggenbuech, B.; Stieger, B.; Foguet, M.; Luebbert, H.; Meier, P.J.  
C:Natl. Acad. Sci. U.S.A. 88, 10629-10633, 1991  
Title: Functional expression cloning and characterization of the hepatocyte Na(+)/bile  
A:Reference number: A41601; MUID:92073340; PMID:1961729  
A:Accession: A41601  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-362 <HMG>  
A:Cross-references: GB:M77429  
C:Keywords: transmembrane protein

	Query Match	28.3%;	Score 559.5;	DB 2;	Length 362;
	Best Local Similarity	37.2%;	Pred. No. 1.4e-38;		
	Matches	133;	Conservative 69;	Mismatches 135;	Gaps 9
Qy	10	ACPANSSEEEELPVGLVEHGNLELFTVVSTVMGMLLMESLGCSVEIRKLWHSRRPWGIA	69		
Dd	7	SAPFNFS---LPFGFG-HRATDKALSIIILVLMLLIMLSIGCTMEFISKAKHLWKPKGYI	62		
Qy	70	VGLLCQFLGMPEFTAYLIAAISLSPKPOVAIVLIMGCCPGGTISNFTFTVDGDMDLSISM	129		
Dd	63	VALVAQFGIMPLAALFLGKI FHLNSIEALAILI CGCSFGGNLSNFTFLAMKGDMNLSIVM	122		
Qy	130	TTGSTVAALGMMPICLIYLT---WSWSIQONLTIPYQNIGITVLCLTTPAFGVGVTVYRW	186		

[illegible]

Query Match	27.9%;	Score 553;	DB 2;	Length 349;
Best Local Similarity	36.0%;	Pred. No. 4.7e-38;		
Matches 124;	Conservative 77;	Mismatches 109;	Indels 34;	Gaps 10
QY	31	ELVTVTVSTVMGILLMPSLGSVEIRKLWGHIRRPNGIAVGLLQCQGLMPETAYLLAISF	90	
DB	24	DLAUSVILVFMFLMISLGCITMBSFKIAHLWPKGLAALVAQIGIMPLFAVLGKVF	83	
QY	91	SLKPQQAIAVLIMGCCPGGTISNIFTPEWDDDLDSISMTTCSVTAALGMPPLCIYLYT-	149	
DB	84	RLKNEALAILVCSPGGLSNVFSLAMKGDWNLISIVMTTCSFPCALGMPPLLIYYSR	143	
QY	150	--MSWSLQOONUTIPYQNIIGITLVCLTTPVAPGVVYVVRMPKQSKIILKIGAVVGVLIV	207	
DB	144	GIYDGDLDK--VPYKGVIVISLVLLVLPCTIGIVLAKSRPQVVRVYKGMII-----ILL	197	
QY	208	VAVAGVLAKGSWNSDI-----TLTITSIPIPLIGHVTGFLA-ALPHTQSMQRC-RTIS	259	
DB	198	CSAVTVTVLSAINVGKSIWFAMTPLLIATSTSMPIGFLGIVLSALFCLNG--RCRRIVS	255	
QY	260	LETGAQNTQMCTIMLQSLFAEHLVQMLSPPLAYGLFQLIDGFLIVAAVQTYKRRLLKNKH	319	
DB	256	NETGQNVQLCSTILNVAFPVEVIGLPFFPPLLYMFIQLGEGLLIATFWCYE-KPKTPK	314	
QY	320	GKNSGGCTEVCHTRKTSSTSSRETNAPLEVNNEGAIITPGPGPMDOC	363	
DB	315	DK-----TKMITYTAATT-----EETIPGALNGITYKGDCD	344	

RESULT 5  
S01696  
gene p3 protein - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 05-Nov-1999  
C:Accession: S01696  
R:Alcalay, M.; Toniolo, D.  
Nucleic Acids Res. 16, 9527-9543, 1988





QY 270 CITMLQLSFT 279  
Db 298 GFLLAQKFT 307

RESULT 11  
F83236  
A:Gene: PA3264 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F83236  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
Reference number: AB2950; MUID:20437337; PMID:10984043  
Accession: F83236  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-311 <STO>  
A:Cross-references: GB:AE004091; NID:g9949388; PIDN:AAG06652.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA3264  
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.6%; Score 269.5; DB 2; Length 311;  
Best Local Similarity 25.7%; Pred. No. 9.2e-15;  
Matches 75; Conservative 74; Mismatches 116; Indels 27; Gaps 8;

QY 32 LVFTVSTVMGLMFLSGSVEIRKLSHRRPWGIAVGLLCOFLMPFTAYLLAISFS 91  
Db 34 LPLTAIAPLGLVNFGLTKGEDPREVAHPRVLVGLVLAQVINGPLANLLCRLLQ 93

QY 92 LKPVQIAVLINGCCPGGTISNFTFWVDGMDLSMTTCTSTVAALGMPLCIYLYTWS 151  
Db 94 LPAEIAVGVLVCCPGGTASNVMTLSRGDVALSVATSVTTLLAPLVTPALVWLLASA 153

QY 152 WSLQNLITPQNICITLV-CLTIPVAVGVVYVYVYVYVYVYVYVYVYVYVYVYV 210  
Db 154 W-----LPVSFAAMFLSLQVVLVPIALGLLAQRLGERTQVAEVLPLV-SVFSIVVII 207

QY 211 AGVLAKGSWNSDITLLTISFTF-----PLIGHVTGFLALFTHQSQRCTISLEGA 264  
Db 208 AAVVAASQARTAESGLLIMAVVHLHNGFGLLGYLTGKTGMLPAQR-----KALAEVGM 263

QY 265 QNIMCITMLQLSFTAHLVQMLSPPLA-YGLFQIDGLFLIVAAVYQTYKRRL 315  
Db 264 QN-----SGLGAALANAFSLAAPSALFSVWHNLSGSLAALF-----RRL 306

RESULT 12  
B81168  
A:Gene: NMB0705 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: B81168  
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755; PMID:10710307  
Accession: B81168  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-315 <TET>  
A:Cross-references: GB:AE002425; GB:AE002098; NID:g7225930; PIDN:AAFA1122.1; PID:g722593  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:

A:Gene: NMB0705  
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.5%; Score 266.5; DB 2; Length 315;  
Best Local Similarity 26.6%; Pred. No. 1.6e-14;  
Matches 81; Conservative 65; Mismatches 102; Indels 57; Gaps 10;

QY 41 MWGLMFLSGSVEIRKLSHRRPWGIAVGLLCOFLMPFTAYLLAISFSKPVQAIAY 100  
Db 43 LLGIIMFGMGLTKPSDFDILFKHPKVIIGVIAQFAIMPATAWLLSKLLNLPABIAVGV 102

QY 101 LIMCCPGGTISNFTFWVDGMDLSMTTCTSTVAALGMPLCIYLYVTSWSLQONLTI 160  
Db 103 ILVCCPGGTASNVMTYLARGNVALSVAVTSVLSPLLP-AIFLML-----AGEMLEI 157

QY 161 PYQNICITLV-CLTIPVAVGVVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 201  
Db 158 QAAGMLMSIVKMWLLPIVLGLVHKVLSKTEKLTALPLVSVAAIVLIIGAVVGASKG 217

QY 202 ----GVLLLVAVAGVVLAKGSWNSDITLLTISFTFPLIGHVTGFLALFTHQSQRCT 257  
Db 218 IMESGLLIFAV-----VVLHNG-----IGYLLGFFAAKWTGLPDAQKT 256

QY 258 ISLETGAQNICITMLQLSFTAHLVQMLSPPLA-YGLFQIDGLFLIVAAVYQTYKRRLK 316  
Db 257 LTIEVGMQNSGLAALAAAHFAAPV---AVPGALFSVWHNLSGSLA---TYWAAKA 309

QY 317 NKHCK 321  
Db 310 GKHKK 314

RESULT 13  
B81937  
A:Gene: NMB0705 [imported] - Neisseria meningitidis (strain Z2491)  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: B81937  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagers, K.; Leather, S.; Mounle, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: AB1775; MUID:20222556; PMID:10761919  
Accession: B81937  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-315 <PAR>  
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84186.1; PID:g737962  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMB0909  
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.4%; Score 265.5; DB 2; Length 315;  
Best Local Similarity 25.9%; Pred. No. 2e-14;  
Matches 79; Conservative 68; Mismatches 101; Indels 57; Gaps 10;

QY 41 MWGLMFLSGSVEIRKLSHRRPWGIAVGLLCOFLMPFTAYLLAISFSKPVQAIAY 100  
Db 43 LLGIIMFGMGLTKPSDFDILFKHPKVIIGVIAQFAIMPATAWLLSKLLNLPABIAVGV 102

QY 101 LIMCCPGGTISNFTFWVDGMDLSMTTCTSTVAALGMPLCIYLYVTSWSLQONLTI 160  
Db 103 ILVCCPGGTASNVMTYLARGNVALSVAVTSVLSPLLP-AIFLML-----AGEMLEI 157

QY 161 PYQNICITLV-CLTIPVAVGVVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 201  
Db 158 QAAGMLMSIVKMWLLPIVLGLVHKVLSKTEKLTALPLVSVAAIVLIIGAVVGASKG 217

QY 202 ----GVLLLVAVAGVVLAKGSWNSDITLLTISFTFPLIGHVTGFLALFTHQSQRCT 257  
Db 218 IMESGLLIFAV-----VVLHNG-----IGYLLGFFAAKWTGLPDAQKT 256

